

Relationships of a new fossorial Microcambevinae catfish species from southern Brazil supporting multiple dorsal-fin losses in *Listrura* (Siluriformes, Trichomycteridae)

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Abstract

Extreme reduction or loss of fins is a common evolutionary feature in fossorial and semifossorial trichomycterids. Here, we analyse the possible occurrence of independent evolutionary events of dorsal fin loss in *Listrura*, a genus of fossorial species endemic to the Atlantic Forest of eastern Brazil, in a molecular phylogenetic context involving all species of the genus, including three nominal species lacking a dorsal fin and another one that is described here. Ancestral state reconstruction analysis indicated the occurrence of three independent events of dorsal fin loss: one in the subgenus *Listrura* (*L. menezesi*) and two in the subgenus *Prolistrura*, in *L. depinnai* and in the clade comprising *L. boticario* and the new species. Osteological comparisons indicate that there are no intermediate stages in the genus; species either possess a well-developed dorsal fin or completely lack both the fin and its internal skeletal support. It was not possible to identify distinct environmental characteristics or ecological preferences between species with and without a dorsal fin. The new species is distinguished from *L. boticario*, its hypothesised sister species, by a different colour pattern, a different number of caudal-fin procurrent rays and interopercular odontodes, and a larger eye.

Key Words

Ancestral state reconstruction, Atlantic Forest, biodiversity, molecular systematics

Introduction

Adaptation to life in fossorial environments is a frequent evolutionary event among teleost fishes, with fossorial species commonly exhibiting an increase in the number of vertebrae and a reduction or loss of fins (e.g., Yamada et al. 2009; Britz et al. 2016; Anoop et al. 2019; Costa and Katz 2021). These two types of adaptations are commonly found in catfishes of the family Trichomycteridae and are particularly pronounced in representatives of the subfamilies Glanapteryginae (Myers 1927, 1944; de Pinna 1989; Costa and Bockmann 1994; Schaefer et al. 2005; de Pinna and Zuanon 2013) and Microcambevinae (Costa and Katz 2021 and included references; de Medeiros et al. 2024 and included

references). In *Listrura* de Pinna, 1988, a genus of small fossorial catfishes, there is a high number of vertebrae (43–55); the pectoral fin is reduced, having a maximum of four rays; the pelvic fin is always absent; and the dorsal fin is absent in three species (Villa-Verde and Costa 2006; Costa and Katz 2021; Villa-Verde et al. 2022). The independent acquisition of a large number of vertebrae, associated with the independent loss or extreme reduction of fins in different trichomycterid lineages, has led to the erroneous placement of some taxa, such as the allocation of the genus *Listrura* in Glanapteryginae (de Pinna 1988). However, with the widespread use of molecular data in phylogenies, relationships among highly morphologically convergent trichomycterid lineages are being elucidated (Costa et al. 2020a; Ochoa

et al. 2020). Phylogenetic studies have supported *Listrura* as a member of a clade endemic to the Atlantic Forest of eastern Brazil, comprising the subfamily Microcambevinae (Costa et al. 2020a). *Listrura* presently comprises a total of 13 species, among which three lack a dorsal fin (Costa and Katz 2021). Morphological data have suggested that dorsal fin loss occurred independently in each of the three *Listrura* species lacking this fin (Costa and Katz 2021). Here, we first evaluate the evolution of dorsal fin loss in *Listrura* based on a molecular phylogeny encompassing all species of the genus, including the three nominal species without a dorsal fin and a fourth one from subtropical southern Brazil that is new and herein described.

Materials and methods

Specimens

Field collections followed procedures approved by CEUA-UFRJ (Ethics Committee for Animal Use of the Federal University of Rio de Janeiro; permit numbers: 065/18 and 084/23) and ICMBio (Instituto Chico Mendes de Conservação da Biodiversidade; permit number: 38553-11). Most specimens were deposited in the ichthyological collection of the Institute of Biology, Federal University of Rio de Janeiro (UFRJ), and some in the Centre of Agrarian and Environmental Sciences, Federal University of Maranhão, Campus Chapadinha (CICCAA). In specimen lists, C&S indicates specimens cleared and stained for osteological examination, and DNA refers to specimens directly fixed in ethanol for molecular analysis. Comparative material is listed in Costa et al. (2023b), with the addition of the following specimens of *Listrura boticario* de Pinna & Wosiacki, 2002, deposited in Museu Nacional, Federal University of Rio de Janeiro, Rio de Janeiro (MNRJ): BRAZIL • 7 ex., 16–40 mm SL; Paraná State: Antonina Municipality: small stream tributary of the Rio Copiuva, Rio Cachoeira basin; 25°19'25"S, 48°40'31"W; about 30 m a.s.l.; 6 April 2008; L. Villa-Verde et al., leg.; MNRJ 32444; 1 ex. (DNA), 37 mm SL; Paraná State: Guarqueçaba Municipality: Rio da Figueira, Rio Morato basin; 25°10'43"S, 48°18'42"W; about 30 m a.s.l.; 8 April 2008; L. Villa-Verde et al., leg.; MNRJ 32442.

Morphological data

Methods for taking and describing morphological characters followed Costa (1992), Bockmann and Sazima (2004), and Costa et al. (2020b) for morphometric and meristic data; Taylor and Van Dyke (1985) for osteological preparations; Arratia and Huaquin (1995) and Bockmann and Sazima (2004) for latero-sensory system nomenclature; and Costa (2021) for bone terminology, with modifications proposed by Kubicek (2022).

DNA extraction, amplification and sequencing

Genomic DNA was extracted from muscle tissue removed from the right side of the caudal peduncle using the DNeasy Blood & Tissue Kit (Qiagen). The DNA product was evaluated by agarose gel electrophoresis. Polymerase chain reaction (PCR) was performed to amplify target DNA sequences using the following oligos: Cytb Siluri F and Cytb Siluri R (Villa-Verde et al. 2012) for mitochondrial encoded cytochrome *b* (*cytb*); FISHF1 and FISHR1 (Ward et al. 2005) for mitochondrial encoded cytochrome c oxidase I (*coxI*); and RAG2 TRICO F and RAG2 TRICO R (Costa et al. 2020a) for recombination activating gene 2 (*rag2*). PCR reactions were carried out in 60 µL volumes containing 5× Green GoTaq Reaction Buffer (Promega), 1.5 mM MgCl₂, 1 µM of each primer, 0.2 mM of each dNTP, 1 U of Promega GoTaq Hot Start polymerase, and 50 ng of genomic DNA. All reactions included negative controls to check for contamination. The PCR thermal cycling profile consisted of initial denaturation at 94 °C for 4 min; 35 cycles of denaturation at 94 °C for 1 min, annealing at 50–58 °C for 1 min, and extension at 73 °C for 1–1.3 min; followed by a final extension at 73 °C for 5 min. PCR products were purified using the Wizard SV Gel and PCR Clean-Up System (Promega). Sequencing reactions were performed using the BigDye Terminator Cycle Sequencing Mix (Applied Biosystems) in 20 µL reaction volumes containing 4 µL BigDye, 2 µL 5× sequencing buffer (Applied Biosystems), 2 µL PCR product (30–40 ng), 2 µL primer, and 10 µL deionised water. The sequencing thermal profile included 35 cycles of 10 s at 96 °C, 5 s at 54 °C, and 4 min at 60 °C. Reading and interpretation of sequencing chromatograms and sequence annotation were performed using MEGA 11 (Tamura et al. 2021). The obtained DNA sequences were translated into amino acid residues to verify the absence of premature stop codons or indels. GenBank accession numbers are provided in Table 1.

Phylogenetic analyses and ancestral state reconstruction

Each gene dataset was aligned using the Clustal W algorithm (Chenna et al. 2003), implemented in MEGA 11, with no gaps or stop codons detected. The concatenated molecular data matrix comprised 2563 bp (COX1: 657 bp; CYTB: 1083 bp; RAG2: 823 bp). The optimal partition scheme and best-fit evolutionary models were identified using PartitionFinder v.2.1.1 (Lanfear et al. 2016, based on the corrected Akaike Information Criterion (Table 2). Two independent phylogenetic reconstruction approaches were used: Bayesian inference (BI) and maximum likelihood (ML). BI was conducted with BEAST v.1.10.4 (Suchard et al. 2018), employing the Yule Process tree prior (Gernhard 2008), an uncorrelated relaxed lognormal clock model, and two independent Markov chain Monte Carlo (MCMC) runs of 8×10^8 generations, sampled every 1000 generations. Convergence and burn-in were assessed by verifying

Table 1. Terminal taxa included in the molecular phylogeny with corresponding GenBank accession numbers.

	Catalog number	COI	CYTB	RAG2
<i>Trichogenes longipinnis</i>	UFRJ 10295	MK123682.1	MK123704.1	MF431117.1
<i>Trichomycterus nigricans</i>	UFRJ 10989	MN385796.1	MT470415.1	MK123765
<i>Ituglanis boitata</i>	UFRJ 10582	MK123684.1	MK123706.1	MK123758
<i>Microcambeva ribeirae</i>	UFRJ 12179	MN385807.1	OK334290.1	MN385832.1
<i>Listrura tetraradiata</i>	UFRJ 11399	JQ231083.1	JQ231088.1	MN385826.1
<i>Listrura nematopteryx</i>	UFRJ 9268	HM245417.1	HM245425.1	–
<i>Listrura macacuensis</i>	UFRJ 9268	PQ362009	PQ368560	MN385825.1
<i>Listrura macaensis</i>	UFRJ 9693	PQ362010	PQ368561	–
<i>Listrura menezesi</i>	MNRJ 32026	JN830897.1	JN830896	–
<i>Listrura costai</i>	LBDM 551	HM245414.1	HM245421	–
<i>Listrura picinguabae</i>	LBDM 556	HM245416.1	HM245424.1	–
<i>Listrura bernunssa</i>	UFRJ 9465.1	MN385803.1	OK143233.1	MN385827.1
<i>Listrura urussanga</i>	UFRJ 13474	PQ362011	PQ368562	PQ368567
<i>Listrura depinnai</i>	UFRJ 12487.2	PQ362012	PQ368563	–
<i>Listrura camposae</i>	UFRJ 11400.1	PQ362013	PQ368564	PQ368568
<i>Listrura boticario</i>	MNRJ 32442	PP886152	–	–
<i>Listrura elongata</i>	UFRJ 13473	PQ362014	PQ368565	PQ368569
<i>Listrura gyrinura</i>	UFRJ 13352.1	–	PQ368566	–

Table 2. Best-fitting partition schemes with corresponding numbers of base pairs and selected evolutionary models.

Partition	Base pairs	Evolutionary Model
COX1 1 st	219	HKY+I
COX1 2 nd	219	GTR+G
COX1 3 rd	219	TRN+G
CYTB 1 st	361	K80+I+G
CYTB 2 nd	361	HKY+I
CYTB 3 rd	361	GTR+G
RAG2 1 st	275	HKY+G
RAG2 2 nd	274	HKY
RAG2 3 rd	274	HKY

that all parameters reached stationarity and effective sample sizes exceeded 200 using Tracer v.1.7.1 (Rambaut et al. 2018). The consensus tree and Bayesian posterior probabilities were computed with TreeAnnotator v.1.10.4, applying a 25% burn-in. ML analysis was performed using IQ-TREE v.2.2.2.6 (Minh et al. 2020), with node support evaluated using ultrafast bootstrap (UFBoot) (Hoang et al. 2018) and Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT), both with 1000 replicates (Guindon et al. 2010). The BI tree generated by BEAST was analysed in RASP v.4.2 (Yu et al. 2019) using Bayesian Binary MCMC (BBM) analysis for a binary neomorphic character corresponding to the presence or absence of a dorsal fin. Search parameters followed default settings, with the maximum number of areas set to 1.

Results

Phylogeny and evolution of dorsal-fin loss

Phylogenetic analyses yielded identical topologies (Fig. 1), with all major lineages of the genus receiving maximum support values. Ancestral state reconstruction

indicated that dorsal-fin loss originated independently in three intrageneric lineages (Fig. 1), a pattern strongly supported by high posterior probabilities (Suppl. material 1).

Taxonomic accounts

Listrura elongata sp. nov.

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Figs 2–5A–C, Table 3

Holotype. BRAZIL • 1 ex., 58.1 mm SL; Santa Catarina State: Camboriú Municipality: near the village of Cobra Fria and the road Estrada Morro do Gavião, in a stream tributary of the upper Rio Camboriú; 27°06'22"S 48°45'21"W; about 50 m asl; 14 February 2023; C.R.M. Feltrin, leg.; UFRJ 14279.

Paratypes. (all from Santa Catarina State: Camboriú Municipality: Rio Camburiú basin): BRAZIL • 3 ex., 20.5–44.7 mm SL; collected with holotype; UFRJ 14281; 2 ex. (C&S), 40.3–43.8 mm SL; idem; UFRJ 14280; 2 ex. (DNA), 20.2–22.2 mm SL; idem; UFRJ 13473; 2 ex., 26.5–34.8 mm SL; idem; CICCAA 05057; 1 ex., 49.0 mm SL; stream close to the street Rua Manuel Maturino Anastácio; 27°05'32"S, 48°45'22"W; about 30 m asl; 6 February 2023; A. M. Katz and P. J. Vilardo, leg.; UFRJ 13418.

Diagnosis. *Listrura elongata* is distinguished from all other congeners, except *L. boticario*, *L. depinnai*, and *L. menezesi*, by the absence of dorsal fin. *Listrura elongata* is immediately distinguished from *L. boticarioi* and *L. depinnai*, its two congeners of the subgenus *Prolistrura* lacking dorsal fin, by having a different colour pattern of flank, comprising the presence of minute dark brown dots on caudal peduncle and dorsal portion of flank that are smaller than the eye diameter (Fig. 2), vs. dark brown dots larger than the eye diameter (de Pinna and Wosiacki 2002: fig. 1; Villa-Verde et al. 2008, 2013). *Listrura elongata* is

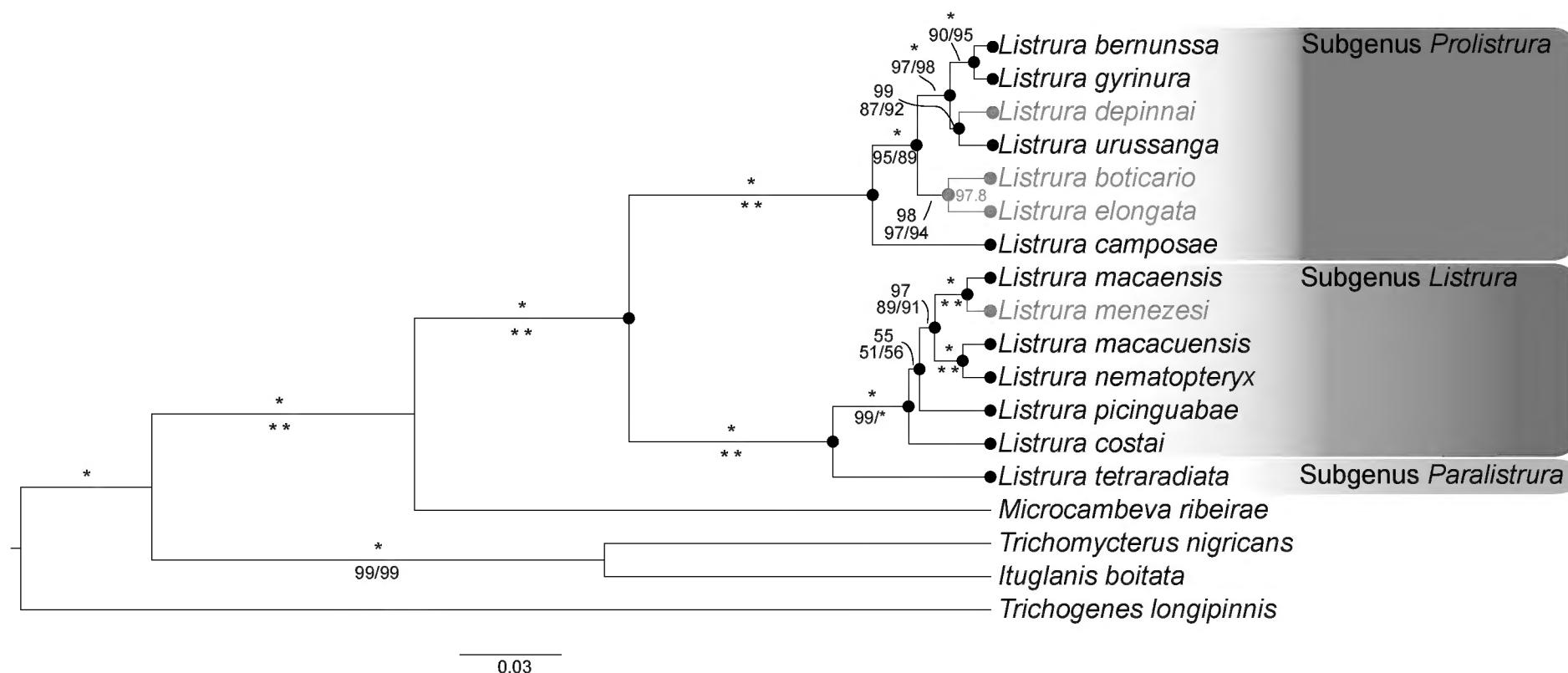


Figure 1. Phylogenetic relationships among species of *Listrura* and four outgroup taxa depicted as an ultrametric tree generated by Bayesian inference (BI) in BEAST, based on a molecular dataset of 2563 base pairs (COX1: 657 bp; CYTB: 1083 bp; RAG2: 823 bp). Numbers above branches indicate posterior probabilities from the BI analysis; numbers below branches indicate Bootstrap and SH-aLRT support values, separated by a slash. Asterisks (*) denote maximum support values. Taxa in red correspond to species lacking a dorsal fin.



Figure 2. *Listrura elongata* sp. nov., UFRJ 14279, holotype, 58.1 mm SL. **A.** Left lateral view; **B.** Dorsal view; **C.** Ventral view.

also distinguished from *L. boticarioi*, its hypothesised sister species (Fig. 1), by having more dorsal (38 vs. 28–30) and ventral (32 or 33 vs. 28) caudal procurent rays, more interopercular odontodes (11–13 vs. eight), and a larger eye (eye diameter 8.5–11.5% of heel length vs. 6.0% of heel length). *Listrura elongata* also differs from *L. depin-*

nai by having more vertebrae (52 vs. 45 or 46), more interopercular odontodes (11–13 vs. four), and a slenderer body (body depth 8.9–11.3% SL vs. 12.3–12.7% SL, caudal peduncle depth 8.4–12.6% SL vs. 14.2–14.5% SL). *Listrura elongata* differs from *L. menezesi* of the subgenus *Listrura* by having more teeth in the premaxilla (20 or 21

vs. 15–18) and dentary (20 vs. 12–16), more dorsal caudal procurrent rays (38 vs. 28–30), and more interopercular odontodes (11–13 vs. five to seven).

Description. External morphology. Morphometric data appear in Table 3. Body elongated, greatest body depth approximately at vertical through area midway distance between pectoral-fin base and anal-fin origin, trunk compressed, dorsal and ventral profiles almost straight (Figs 2, 4). Anus and urogenital papilla in shallow cavity immediately anterior to anal-fin base. Head slightly depressed, subtrapezoidal in dorsal view, anterior profile convex (Fig. 3). Minute skin papillae on anterior portion of ventral surface of head and lips. Eye small, round, positioned on anterior dorsal area of head, nearer snout tip than opercular patch of odontodes, separated by small interspace from posterior nostril (Fig. 3). Posterior nostril approximately equidistant from orbit and anterior nostril (Fig. 3). Mouth subterminal (Fig. 3). Branchial membrane attached to isthmus only at its middle anterior point (Fig. 3).

Barbels relatively long (Fig. 3); nasal barbel reaching between opercular patch of odontodes and area just anterior to it, maxillary barbel reaching between pectoral-fin base and area immediately anterior to it, rictal barbel reaching between posterior limit of interopercular patch of odontodes and pectoral-fin base. Jaw teeth pointed, arranged in two rows. Total premaxillary teeth 20 or 21, outer row 8, inner row 12 or 13; total dentary teeth 20, outer row 8 or 9, inner row 11 or 12. Odontodes pointed (Fig. 5B). Opercular odontodes 6 or 7, interopercular odontodes 11–13. Branchiostegal rays 6. Cephalic latero-sensory system represented by short postorbital canal with 2 pores above opercular patch of odontodes, connected to short lateral line on anterior portion of trunk, with 1 or 2 pores.

Dorsal fin absent. Anal fin small, rounded, total anal-fin rays 8 (ii + 6). Pectoral fin narrow, total pectoral-fin rays 2 or 3, all segmented and unbranched, first ray longer, second ray about one-third to half first ray length, third ray when present rudimentary. Pelvic fin and girdle absent. Caudal fin spatula-shaped, total principal caudal-fin rays 13 (II + 9 + II), total dorsal procurrent rays 38 (xxxvii + I–II), total ventral procurrent rays 32 or 33 (xxxix–xxxii + I).

Osteology. Mesethmoid thin, abruptly widening posteriorly, with narrow and straight cornu (Fig. 5A). Lacrimal nearly rectangular, with pronounced postero-lateral pointed expansion (Fig. 5A). Sesamoid supraorbital small, elliptical (Fig. 5A). Premaxilla broad, sub-triangular in dorsal view, with narrow lateral expansion (Fig. 5A). Maxilla straight, relatively short, slightly shorter than premaxilla, tapering laterally (Fig. 5A). Autopalatine sub-rectangular in dorsal view, lateral margin slightly concave, medial margin weakly sinuous (Fig. 5B). Autopalatine postero-lateral process short, dorsally directed (Fig. 5B). Autopalatine articular facet for mesethmoid wide, without distinctive processes (Fig. 5B). Metapterygoid small, subtrapezoidal (Fig. 5B). Quadratojugal slender, L-shaped, dorsal process small, with short posterior expansion (Fig. 5B). Hyomandibula long, anterior outgrowth narrow, anteriorly tapering and terminating in sharp tip (Fig. 5B). Hyomandibular



Figure 3. Head and anterior portion of trunk of *Listrura elongata* sp. nov., UFRJ 14279, holotype, 58.1 mm SL. **A.** Left lateral view; **B.** Dorsal view; **C.** Ventral view.

articular facet for opercle robust, without distinctive ventral expansion (Fig. 5B). Opercle and interopercle slender; transverse length of opercular odontode patch about half length of dorsal hyomandibular articulation for neuromast, transverse length of interopercular odontode patch about three-fourths that length (Fig. 5B). Preopercle narrow and long (Fig. 5B). Parurohyal with narrow and pointed lateral process and moderate posterior process, its length about two-thirds of length between anterior margin of parurohyal and posterior process base (Fig. 5C). Parurohyal head with prominent anterolateral paired process (Fig. 5C). Middle foramen of parurohyal small, elliptical (Fig. 5C). Vertebrae 52. Ribs 2 or 3. Caudal skeleton comprising two hypural plates in contact, dorsal plate corresponding to hypurals 3–5, ventral plate corresponding to hypurals 1–2 and parhypural. Anal-fin origin at vertical through centrum of 33rd vertebra.

Colouration in alcohol. Dorsum, flank and head pale yellowish grey with minute dark brown dots irregularly arranged (Figs 2, 3). Dots smaller than eye diameter, on dorsum, dorsal portion of flank and caudal peduncle (Fig. 2). Slightly larger dots concentrated on longitudinal midline line of flank anterior to caudal peduncle, longitudinal line on dorsal portion of flank, central and anterior portions of dorsal surface of head, and opercular,

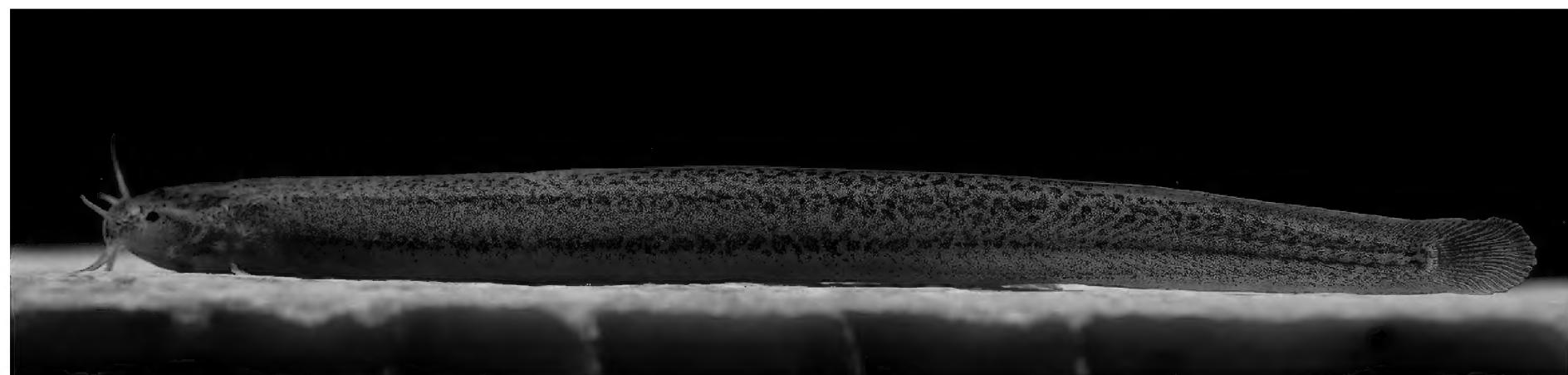


Figure 4. *Listrura elongata* sp. nov., UFRJ 13418, live paratype, 49.0 mm SL.

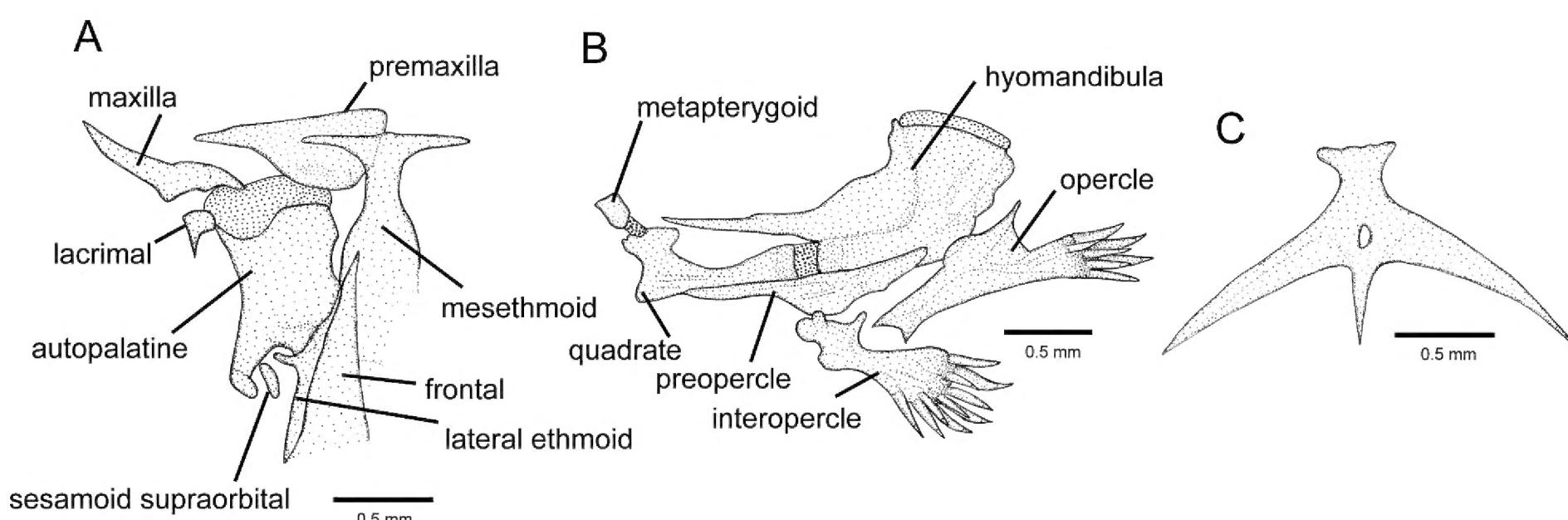


Figure 5. Osteological structures of *Listrura elongata* sp. nov. **A.** Mesethmoidal region and adjacent structures, left and middle portions, dorsal view; **B.** Left jaw suspensorium and opercular series, lateral view; **C.** Parurohyal, ventral view. Larger stippling represents cartilaginous areas.

interopercular, and branchiostegal regions (Figs 2, 3). Ventral surface of head and trunk yellowish white (Figs 2, 3). Dark brown chromatophores concentrated on chin and branchiostegal region (Fig. 3). Fins whitish hyaline, with minute brown chromatophores on anal-fin base and brown pigmentation on middle of caudal fin (Fig. 2).

Colouration in life. Similar to colouration in preserved specimens, with ground colour slightly darker (Fig. 4).

Etymology. From the Latin *elongata* (elongate), referring to the slender and long body of the new species.

Distribution and habitat notes. *Listrura elongata* is only known from the Rio Camboriú basin, an isolated small river basin in the Atlantic Forest of southern Brazil (Fig. 6). It was first found (i.e., a single specimen, UFRJ 13418) in the main channel of the upper Rio Camboriú, inside a plant remnant similar to a fern stem with earthy/clayey material attached to it. Ten days later, the same watercourse was intensively sampled, from 600 m above to 300 m below that collecting point, but no specimen was found, concluding that possibly the plant material was brought by a flood from some upstream tributary. Subsequently, about 15 different watercourses were investigated in neighbouring areas. The species was then found in a small stream tributary of the upper Rio Camboriú, the type locality (Fig. 7). It crosses a still forested segment at its right bank, but just below the type locality, the stream course reaches a deforested area occupied by cattle paddocks, which is followed by a large-scale rice plantation. The type locality is situated on a brief slope generating a

weak water flow. The stream is about 100 cm wide and 1–35 cm deep, with clear water, except in eutrophicated areas, with great concentration of fungi and algae, where the water is turbid. There is a great concentration of amphibious herbs at the site where specimens were collected (Fig. 7). The second collecting point, the type locality, is about 1.5 km away from the first one. Further field studies in neighbouring river basins were unsuccessful in finding other populations of *L. elongata* (see discussion below).

Table 3. Morphometric data of *Listrura elongata* sp. nov.

	Holotype	Paratypes (n = 6)
Standard length (SL)	58.1	32.3–49.0
Percentage of standard length		
Body depth	11.0	8.9–11.3
Caudal peduncle depth	8.6	8.4–12.6
Body width	5.2	6.5–7.2
Caudal peduncle width	1.6	1.7–2.9
Anal-fin base length	5.2	5.1–8.3
Caudal-fin length	13.2	8.9–15.1
Pectoral-fin length	10.4	6.5–11.3
Head length	11.8	11.6–14.8
Percentage of head length		
Head depth	53.9	46.6–52.9
Head width	86.8	81.5–86.6
Snout length	38.2	35.1–41.4
Interorbital width	22.4	19.0–25.8
Preorbital length	6.6	4.9–8.3
Eye diameter	9.4	8.5–11.3

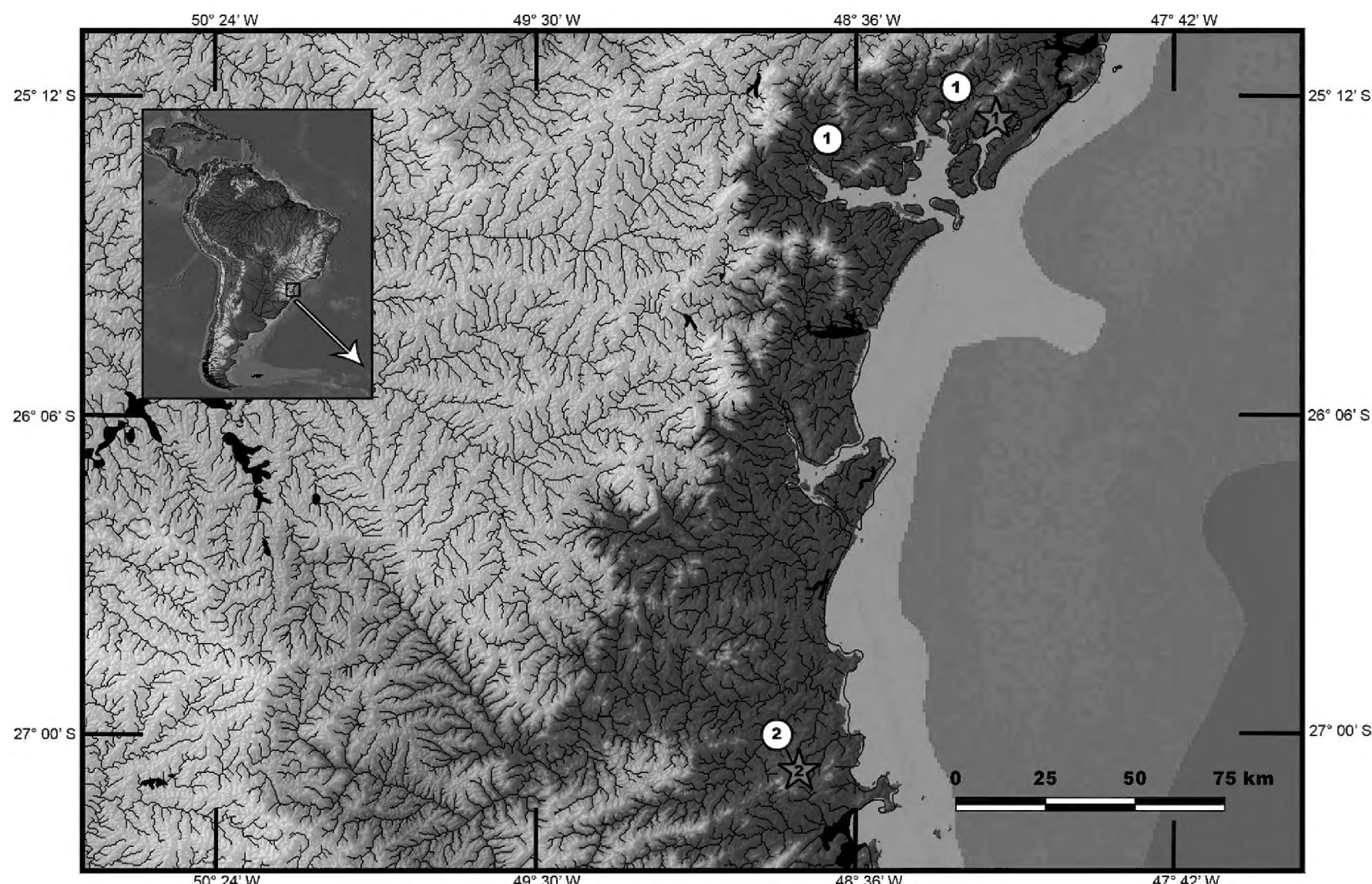


Figure 6. Geographical distribution of *Listrura elongata* sp. nov. (1) and *L. boticario* (2). Stars indicate type localities.



Figure 7. Stream tributary of the upper Rio Camboriú, type locality of *Listrura elongata* sp. nov.

Discussion

Costa and Katz (2021) suggested that dorsal-fin loss in *Listrura* occurred three times independently in the three species then known: once in the subgenus *Listrura* (i.e., *L. menezesi*) and twice in *Prolistrura* (*L. boticario* and *L. depinnai*). However, the hypothesis of independent dorsal-fin loss within *Prolistrura* was based solely on morphological data, as molecular data for *L. boticario* were not available. With the recent publication providing a COX1 sequence for *L. boticario* (Medeiros et al. 2024), that hypothesis has now been corroborated (Fig. 1) and further strengthened by the inclusion of the new species described here, *L. elongata*, which is strongly supported as the sister group of *L. boticario*. Therefore, the present phylogenetic analysis, for the first time including all

species lacking a dorsal fin, corroborates the occurrence of three independent losses within the genus (Fig. 1; see Results). One of the dorsal-fin losses would have occurred in the most recent common ancestor of the clade comprising *L. boticario* and *L. elongata*. These two species occur in coastal streams of southern Brazil, in areas separated by approximately 200 km (Fig. 6). Aquatic biotopes typically inhabited by species of *Listrura* were intensively sampled by one of us (CRMF) in the broad area between the type localities of *L. boticario* and *L. elongata*, but no specimens of either species were found.

Pelvic-fin loss is a frequent evolutionary event among semifossorial and fossorial trichomycterid catfishes. For example, in the *Trichomycterinae*, a diverse clade of semifossorial taxa living on and temporarily burrowing into the stream bottom or marginal vegetation, pelvic-fin loss has occurred independently in different genera (e.g., Fernández and Vari 2000; Fernández and de Pinna 2005; Datovo 2016; Costa et al. 2020c 2023c), including at least three times independently within the same genus, *Cambava* Katz, Barbosa, Mattos & Costa, 2018 (Costa et al. 2023a). In contrast, dorsal-fin loss is a rare event in trichomycterids, occurring only in species with clearly fossorial habits (Schaefer et al. 2005; Costa and Katz 2021). In *Listrura*, our analysis indicated independent loss in three lineages with high probabilistic support (Suppl. material 1). Interestingly, there are no intermediate stages such as extreme fin reduction: either species have a well-developed dorsal fin, with multiple rays, or there are no traces of either the dorsal fin or its internal skeletal support. Furthermore, it was not possible to identify distinct environmental characteristics or ecological preferences

between species with and without a dorsal fin that could be interpreted as factors favouring fin loss, aside from the fossorial habit shared by all species of the genus.

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Supplementary material 1

Ultrametric topology obtained through Bayesian inference in BEAST v1.10.4

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Data type: tif

Explanation note: Coloured circles on the nodes represent ancestral state reconstructions in RASP 4.2: blue indicates presence of dorsal fin; red indicates absence of dorsal fin. Numbers below nodes indicate character state probabilities.

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